

IN THE TITLE:

Please amend the title as follows:

“METHOD OF HANDLING DATABASE FOR BIOINFORMATICS”

IN THE SPECIFICATION:

Please amend the specification as follows:

Beginning on page 1, line 19 running to page 2, line 4, delete the existing paragraph entitled "Description of the background" and replace with the following:

--Description of the background

Successful achievement of human gene projects performed in the early twenty-first century brought about rapid development in all life science fields. Due to completion of the human gene map, studies on ~~the~~ human genes and the structures and functions of human proteins will be actively carried out in post genome ~~genom~~. While a computer stores information represented by 0 and 1, ~~the~~ human genes store ~~stores~~ information of about three billion ~~billions~~ represented by four letters, A, T, G and C. As the studies are performed, a vast amount of digital information is being accumulated and many databases related with bioinformatics, such as SwissProt, GenBank® ~~GenBank~~ and the European Molecular Biology Laboratory (EMBL) ~~EMBL~~, are opened to the public through a web.—

Beginning on page 2, line 5 running through line 9, please delete the existing first paragraph and replace it with the following:

--There are various programs used for searching these bioinformatics databases for appropriate gene information at the request of a user. These programs are classified into a pattern match program (such as ~~FastA~~, BLAST FASTA™, BLAST™ (Basic Local Alignment Search Tool), and CLUSTALW™ ~~Clustal W~~, which search ~~searches~~ for data composed of A, T,

G and C to perform sequence comparison) [,] and a program of predicting a structure from data sequence [,] (such as J-NET™ and J-PRED™ ~~J-NET and J-PRED~~).--

Beginning on page 2, line 17 running through page 3 (renumbered) line 3, please delete the last paragraph and replace it by the following:

--The programs such as FASTA™ and BLAST™ ~~FastA and BLAST~~ are provided to users through a web. A user connects to a server to transmit a protein sequence he/she wants to compare and analyze to the server. Then, the server reads sequences from the database and compares them with the protein sequence requested by the user. These programs operate based on a database. That is, the programs should access the database to read data and respond to a user's request for every user request. In case of FASTA™ ~~FastA~~, for instance, a user transmits a sequence he/she wants to compare/analyze to FASTA™ ~~FastA~~ server. The transmitted sequence is compared with sequences stored in the database to check similarity, and sequences having similarity of higher than a predetermined value are returned to the user. Here, the server accesses the database for each user's request.—

Beginning on page 4 (renumbered), line 8 running through line 11, please delete the existing paragraph and replace it with the following:

--The average time taken for one user to connect to the server and compare one sequence ~~sequences~~ with the sequences of the database, C_{avg}^0 , which corresponds to the sum of the time of equation (a) and the time of equation (2), can be represented as follows.

$$C_{avg}^0 = C_{DB} + C_{seq} = C_{io}N_b + C_{cpu}N_b = (C_{io} + C_{cpu})N_b --$$

Beginning on page 5 (renumbered), line 10 running through line 16, please delete the existing paragraph and replace it with the following:

--Accordingly, the present invention has been made in view of the above problems, and it is an object of the present invention is to provide a database handling a method in which, when a user requests the database server to process comparison of a bioinformatics-related sequence, the server does not wait for completion of processing of a previous user request being processed but processes the new user request and the previous user request simultaneously, so that the server can access the database only once for each user request, thereby saving system cost and response time.—

Beginning on page 8 (renumbered), line 11 running through line 15, please delete the existing paragraph and replace it with the following:

--In the meantime ~~mean-time~~, the sequence comparison/analysis program 3-2 initializes a specific parameter k to set in association with the operation thereof. At step S21, when there is a user-requested sequence in the queue, the sequence comparison/analysis program 3-2 reads the kth sequence from the database 4 at step S22, and then compares it with all of sequences stored in the queue at step S23 (Third stage).—

Beginning on page 9 (renumbered), line 1 running through line 5, please delete the existing paragraph and replace it with the following:

--As described above, the present invention simultaneously processes the currently requested sequence and the previously ~~previous~~ requested sequence ~~being processed~~, ~~simultaneously~~. This is possible because all of the data of the database can be processed irrespective of the data processing order since all of the sequences of the database are generally

searched in sequence search of bioinformatics and there is no dependence among the data items of the bioinformatics database.--

Beginning on page 12 (renumbered), line 14 running through line 20, please delete the existing paragraph and replace it with the following:

--The database GenBank® ~~GenBank~~ (Protein Sequence Database of Rip International Release 72.02), actually being used in bioinformatics, was managed by Los ~~Ros~~ Alamos research institute in support of National Institute of Health in 1981, and transferred to National Center for Biotechnology Information (NCBI) under the control of National Library of Medicine in 1992. With this GenBank® ~~GenBank~~, cytochrome that acts upon oxidization and reduction of cells, one of human proteins, was used as a user-requested sequence. As a result, C_{DB} was 3.99sec and C_{seq} , the cost required for comparing the user-requested sequence with all of sequences of the database, was 19.98 sec.--